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**INFORMATION DISCLOSURE STATEMENT BY APPLICANT**  
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Application Number: 10/057,552  
Filing Date: January 25, 2002  
First Named Inventor: MAYO, Stephen L. et al.  
Group Art Unit: 1645  
Examiner Name: not yet assigned  
Attorney Docket Number: A-65353-9/RFT/RMS/RMK

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### U.S. PATENT DOCUMENTS

Examiner Initials*	Cite No. <sup>1</sup>	U.S. Patent Document		Name of Patentee or Applicant of Cited Document	Date of Publication of Cited Document MM-DD-YYYY	Pages, Columns, Lines, Where Relevant Passages or Relevant Figures Appear
		Number	Kind Code <sup>2</sup> (if known)			
✓	A1	4,939,666		Hardman, K.D.	07/03/1990	
	A2	5,241,470		Lee et al.	08/31/1993	
	A3	5,527,681		Holmes	06/18/1996	

### FOREIGN PATENT DOCUMENTS

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		Office <sup>3</sup>	Number <sup>4</sup> (if known)	Kind Code <sup>2</sup> (if known)				
✓	B1	WO	95/22625	A1	AFFYMAX TECHNOLOGIES N.V.	08/24/1995		
	B2	WO	98/32845	A1	BIOINVENT INTERNATIONAL AB	07/30/1998		
	B3	WO	00/23564	A2	XENCOR, INC.	04/27/2000		
	B4	WO	00/68396	A2	XENCOR, INC.	11/16/2000		
	B5	WO	00/68396	A3	XENCOR, INC.	11/16/2000		
	B6	WO	01/59066	A2	XENCOR, INC.	08/16/2001		
	B7	WO	01/59066	A3	XENCOR, INC.	08/16/2001		

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✓	C1	Brenner and Berry, A., et al., "A quantitative methodology for the de novo design of proteins", Protein Sci. 3:1871-1882 (Oct. 1994).	
	C2	Borman, "Proteins to Order," Chemical and Engineering Newsletter (C&EN) Oct. 6, 1997, 9-10 (1997).	
	C3	Bowie, J.U., et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions", Science vol.247:1306-1310 (Mar. 1990).	
	C4	Bowie, J.U., et al., "A Method to Identify Protein Sequences that Fold into a Known Three-Dimensional Structure", Science vol.253:164-170 (Jul. 1991).	
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<b>INFORMATION DISCLOSURE STATEMENT BY APPLICANT</b> (Use as many sheets as necessary)		Application Number	10/057,552
		Filing Date	January 25, 2002
		First Named Inventor	MAYO, Stephen L. et al.
		Group Art Unit	1645
		Examiner Name	not yet assigned
		Attorney Docket Number	A-65353-9/RFT/RMS/RMK
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	C6	Connolly, M.L., "Solvent-Accessible Surfaces of Proteins and Nucleic Acids", Science vol.221(4612):709-713 (Aug. 1983).	
	C7	Cornell et al., "A Second Generation Force Field for the Simulation of Proteins, Nucleic Acids, and Organic Molecules," J. Am. Chem. Soc., 117:5179-5197 (1995).	
	C8	Dahiyat, B.I., et al., "Automated design of the surface positions of protein helices", Protein Science 6:1333-1337 (Jun. 1997).	
	C9	Dahiyat et al., "Protein design automation," Caltech Biology Annual Report, 172 (1995).	
	C10	Dahiyat, B.I., et al., "Proteins from Scratch", press digest email by Science (Sep. 26, 1997).	
	C11	Dahiyat et al., "Protein Design Automation," Meeting Abstract; Protein Science vol. 4, Suppl. 2, 83 (1995).	
	C12	Dahiyat et al., "Protein design Automation," Poster Sessions, Protein Science vol.5, Suppl. 1, 22-23 (1996).	
	C13	Dahiyat et al., "De Novo Protein Design: Fully Automated Sequence Selection," Science, 278:82-87 (1997).	
	C14	Dahiyat et al., "Probing the Role of Specificity in Protein Design," Caltech Biology Annual Report, 160-161 (1996).	
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	C16	Dahiyat, B.I., et al., "First fully automatic design of a protein achieved by Caltech scientists", new press release (Oct. 1997).	
	C17	Dalal, S., et al., "Protein alchemy: Changing .beta.-sheet into .alpha.-helix", Nature Struc. Biol. vol.4(7):548-552 (Jul. 1997).	
	C18	DeGrado, W., "Proteins from Scratch," Science, 278:80-81 (1997).	
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	C20	Desjarlais et al., "New strategies in protein design," Current Opinion in Biotechnology :460-466 (1995).	
	C21	Desmet, J., et al., "The 'Dead End Elimination' Theorem: A New Approach to the Side Chain Packing Protein", from "The Protein Folding Problem and Tertiary Structure Prediction" Ch.10:1-49 (1994).	
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		Examiner Name	not yet assigned
		Attorney Docket Number	A-65353-9/RFT/RMS/RMK
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	C23	Desmet et al., "Theoretical and Algorithmical Optimization of the Dead-End Elimination Theorem," Proceedings of the Pacific Symposium on Biocomputing '97, 122-133 (1997).	
	C24	Dunbrack Jr., R.L., et al., "Conformational analysis of the backbone-dependent rotamer preferences of protein sidechains", Struc. Biol. vol.1(5):334-340 (May 1994).	
	C25	Eisenberg, D., et al., "Solvation energy in protein folding and binding", Nature vol.319:199-203 (Jan. 1986).	
	C26	Gallop et al., "applications of Combinatorial Technologies to Drug Discovery. 1. Background and Peptide Combinatorial Libraries," Journal of Medicinal Chemistry Vol. 37, No. 9 (April 29, 1994), 1233-1251.	
	C27	Goldstein, R.F., "Efficient Rotamer Elimination Applied to Protein Side-Chains and Related Spin Glasses", Biophys. Jour. vol.66:1335-1340 (May 1994).	
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	C29	Harbury et al., "Repacking protein cores with backbone freedom: Structure prediction for coiled coils," Proc. Natl. Acad. Sci. USA, 92:8408-8412 (1995).	
	C30	Harbury et al., "High-Resolution Protein Design with Backbone Freedom," Science, 282:1462-1467 (1998).	
	C31	Hellinga, H.W., et al., "Construction of New Ligand Binding Site in Proteins of Known Structure", J. Mol. Biol. 222:763-785 (1991).	
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	C35	Hurley et al., "Design and Structural Analysis of Alternative Hydrophobic Core Packing Arrangements in Bacteriophage T4 Lysozyme," J. Mol. Biol., 224:1143-1159(1992).	
	C36	Jones, D.T., "De novo protein design using pairwise potentials and a genetic algorithm", Protein Science 3:567-574 (1994).	
	C37	Kochl et al., "De Novo Protein Design. I. In Search of Stability and Specificity," J. Mol. Biol., 293:1161-1181 (1999).	

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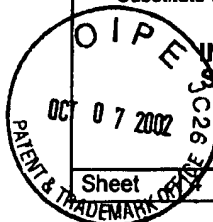
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		First Named Inventor	MAYO, Stephen L. et al.
		Group Art Unit	1645
		Examiner Name	not yet assigned
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<i>[Signature]</i>	C38	Kono et al., "Energy Minimization Method Using Automata Network for Sequence and Side-Chain Conformation Prediction from Given Backbone Geometry," Proteins: Structure, Function, and Genetics, 19:244-255 (1994).	
	C39	Kortemme et al., "Design of a 20-Amino Acid, Three-Stranded $\beta$ -Sheet Protein," Science, 281:253-256 (1988).	
	C40	Lam, Kit S., "Application of Combinatorial Library Methods in Cancer Research and Drug Discovery," Anti-Cancer Drug Design (1997), 12, 145-167.	
	C41	Lasters et al., "Enhanced dead-end elimination in the search for the global minimum energy conformation of a collection of protein side chains," 1995, Protein Engineering, vol. 8, No. 8, pp. 815-822.	
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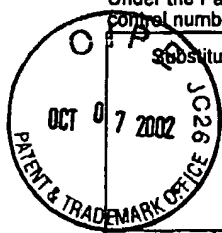
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